Please cancel claims 1-42 and add the following:

43 (New):   A polypeptide selected from the group consisting of:

a)   a polypeptide comprising the amino acid sequence SEQ ID NO: 2, 4 or 6 or a peptide fragment with a minimum length of 6 amino acids,
     whereby in the polypeptide comprising the amino acid sequence SEQ ID NO: 2, the tyrosine residue at position 88 and/or the tyrosine residue at position 89 in SEQ ID NO: 2 is/are phosphorylated, or
whereby in the polypeptide comprising the amino acid sequence SEQ ID NO: 4, the tyrosine residue at position 77 in SEQ ID NO: 4 is phosphorylated, or
whereby in the polypeptide comprising the amino acid sequence SEQ ID NO: 6, the tyrosine residue at position 91 in SEQ ID NO: 6 is phosphorylated;

b)   a polypeptide
comprising the amino acid sequence SEQ ID NO: 2, 4 or 6 or
comprising the amino acid residues 1 to 95 of SEQ ID NO: 2 or comprising the amino acid residues 1 to 85 of SEQ ID NO: 4 or comprising the amino acid residues 1 to 100 of SEQ ID NO: 6 or
comprising the amino acid residues 50 to 95 of SEQ ID NO: 2 or comprising the amino acid residues 38 to 85 of SEQ ID NO: 4 or comprising the amino acid residues 50 to 100 of SEQ ID NO: 6
characterized in that in the polypeptide derived from the polypeptide with the amino acid sequence SEQ ID NO: 2, the amino acid residue at position 88 and/or position 89 in SEQ ID NO: 2, or
in the polypeptide derived from the polypeptide with the amino acid sequence SEQ ID NO: 4, the amino acid residue at position 77 in SEQ ID NO: 4 or
in the polypeptide derived from the polypeptide with the amino acid sequence SEQ ID NO: 6, the amino acid residue at position 91 in SEQ ID NO: 6
is a non-phosphorylatable amino acid residue, preferably a phenylalanine residue;
or a peptide fragment with a minimum length of 6 amino acids of a polypeptide comprising the amino acid sequence SEQ ID NO: 2, 4 or 6, characterized in that in the peptide fragment of a polypeptide comprising the amino acid sequence SEQ ID NO: 2, the peptide fragment comprises at least one of the flanking amino acid residues of the amino acid residue at position 88 or 89 in

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SEQ ID NO: 2 and the residue at position 88 and/or the residue at position 89 in SEQ ID NO: 2 is a non-phosphorylatable amino acid residue, preferably a phenylalanine residue, or

in the peptide fragment of a polypeptide comprising the amino acid sequence SEQ ID NO: 4, the peptide fragment comprises at least one of the flanking amino acid residues of the amino acid residue at position 77 in SEQ ID NO: 4 and the residue at position 77 in SEQ ID NO: 4 is a non-phosphorylatable amino acid residue, preferably a phenylalanine residue, or

in the peptide fragment of a polypeptide comprising the amino acid sequence SEQ ID NO: 6, the peptide fragment comprises at least one of the flanking amino acid residues of the amino acid residue at position 91 in SEQ ID NO: 6 and the residue at position 91 in SEQ ID NO: 6 is a non-phosphorylatable amino acid residue, preferably a phenylalanine residue; or

c)   a variant or peptidomimetics thereof.

44 (New):   A polypeptide according to claim 43, item a), comprising the amino acid sequence SEQ ID NO: 2, whereby the tyrosine residues at position 88 and/or the tyrosine residue at position 89 in SEQ ID NO: 2 are phosphorylated and whereby the serine residue at position 10 and/or 12 and/or the threonine residue at position 157 and/or the threonine residue at position 187 in SEQ ID NO: 2 are phosphorylated.

45 (New):   A variant or peptidomimetics according to claim 43, item c), comprising the amino acid sequence SEQ ID NO: 2, whereby the tyrosine residues at position 88 and/or the tyrosine residue at position 89 in SEQ ID NO: 2 are phosphorylated and whereby the serine residue at position 10 and/or 12 and/or the threonine residue at position 157 and/or the threonine residue at position 187 in SEQ ID NO: 2 are phosphorylated.

46 (New):   A peptide fragment according to claim 43, item a), with a minimum length of 10 amino acids, preferably with a minimum length of 15 amino acids.

47 (New):   A variant or peptidomimetics according to claim 43, item c), with a minimum length of 10 amino acids, preferably with a minimum length of 15 amino acids.

48 (New):   A nucleic acid molecule encoding a polypeptide according to claim 43, item b).

49 (New):   The nucleic acid molecule of claim 48, being contained in a vector.

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50 (New):   The nucleic acid molecule of claim 48, being contained in a virus particle.

51 (New):   The nucleic acid molecule of claim 48, being contained in a mammalian cell.

52 (New):   An isolated antibody which specifically binds to a polypeptide according to claim 43 and which has less than 10 % cross reactivity with the corresponding non-phosphorylated polypeptide or corresponding non-phosphorylated peptide fragment.

53 (New):   The antibody of claim 52, wherein the antibody is a monoclonal antibody.

54 (New):   The antibody of claim 53, wherein the monoclonal antibody is produced by the hybridoma cell line Mab<p27kip>15 or Mab<p27kip>388.

55 (New):   The antibody of claim 52, wherein the antibody is a polyclonal antibody.

56 (New):   The hybridoma cell line Mab<p27kip>15 or Mab<p27kip>388 as deposited with the DSMZ.

57 (New):   A method for treating a patient, involving administering to a patient a polypeptide according to claim 43.

58 (New):   The method of claim 57, wherein said treating is the treatment of hyperproliferative disease.

59 (New):   The method of claim 58, wherein the hyperproliferative disease is a cancer.

60 (New):   A pharmaceutical composition comprising a polypeptide according to claim 43 and a pharmaceutically acceptable carrier.

61 (New):   A method of determining whether or not a human cancer cell containing patient sample has potential for tumor progression, the method comprising comparing:
   a) the level of expression a polypeptide according to claim 43 in the patient sample; and
   b) the normal level of expression the polypeptide or the peptide fragment in a sample from a

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control subject not afflicted with cancer;

and an at least 1.5 fold difference or a less than 0.75 fold difference between the level of expression of the polypeptide or the peptide fragment in the patient sample and the normal level of the polypeptide or the peptide fragment in the sample from a control subject not afflicted with cancer is an indication that the patient sample has potential for tumor progression,

62 (New):   The method of claim 61, wherein the presence or the level of expression of said polypeptide or said peptide fragment is detected using a reagent which specifically binds with said polypeptide or peptide fragment.

63 (New):   The method of claim 62, wherein the reagent is an antibody, an antibody derivative, and an antibody fragment.

64 (New):   The method of claim 61, wherein the human cancer cell is a breast cancer cell, a colorectal cancer cell or a leukaemia cell, preferably a Philadelphia chromosome positive leukaemia cell, more preferably a chronic myeloid leukaemia cell or an acute lymphoblastic leukaemia cell.

65 (New):   The method of claim 61, wherein the sample is a tissue sample, blood or blood derived cells, primary cell cultures from patients, stool, lymph or a tissue-associated fluid or urine.

66 (New):   A method of selecting a composition for inhibiting the progression of cancer in a patient, the method comprising:
a) providing a sample comprising cancer cells from the patient;
b) separately exposing aliquots of the sample in the presence of a plurality of test compositions;
c) comparing the level of expression of the polypeptide according to claim 43 in each of the aliquots; and
d) selecting one of the test compositions which alters the level of expression of the polypeptide in the aliquot containing that test composition, relative to other test compositions,

67 (New):   The method of claim 66, wherein the presence or the level of expression of said polypeptide or said peptide fragment is detected using a reagent which specifically binds with

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said polypeptide or peptide fragment.

68 (New):   The method of claim 67, wherein the reagent is an antibody, an antibody derivative, and an antibody fragment.

69 (New):   The method according to claim 66, wherein the human cancer cell is a breast cancer cell, a colorectal cancer cell or a leukaemia cell, preferably a Philadelphia chromosome positive leukaemia cell, more preferably a chronic myeloid leukaemia cell or an acute lymphoblastic leukaemia cell.

70 (New):   The method according to claim 66, wherein the sample is a tissue sample, blood or blood derived cells, primary cell cultures from patients, stool, lymph or a tissue-associated fluid or urine.

71 (New):   A method to predict which patients will respond to a tyrosine kinase inhibitor drug in patients with a disorder whose underlying pathology involves the discontrol of a tyrosine kinase comprising:
a) contacting a sample from a patient with an antibody according to claim 52;
b) determining the level of phosphorylated polypeptide bound by the antibody of step a);
c) comparing the level of phosphorylated polypeptide determined in step b) for the sample with the level of phosphorylated protein in a reference sample, thereby detecting the responsiveness to a tyrosine kinase inhibitor drug in patients with a disorder whose underlying pathology involves the discontrol of a tyrosine kinase.

72 (New):   The method according to claim 71, wherein the reference sample is a sample from a patient who responds to the tyrosine kinase inhibitor drug.

73 (New):   The method according to claim 71, wherein the tyrosine kinase inhibitor is imatinib mesylate.

74 (New):   The method according to claim 71, wherein the patients with a disorder whose underlying pathology involves the discontrol of a tyrosine kinase are cancer patients.

75 (New):   The method according to claim 74, wherein the cancer patients are Philadelphia

chromosome positive leukaemia patients preferably, chronic myeloid leukaemia patients or acute lymphoblastic leukaemia patients.

76 (New):   A method of deriving a candidate agent, said method comprising:

a) contacting a sample containing cancer cells, with said candidate agent;

b) determining the level of expression of the polypeptide according to claim 43 in the sample contacted with the candidate agent and determining the level of expression of the polypeptide in a sample not contacted with the candidate agent;

c) observing the effect of the candidate agent by comparing the level of expression of the polypeptide or the peptide fragment in the sample contacted with the candidate agent and the level of the polypeptide or the peptide fragment in the sample not contacted with the candidate agent;

d) deriving said agent from said observed effect;

wherein an at least 1.5 fold difference or a less than 0.75 fold difference between the level of expression of the polypeptide or the peptide fragment in the sample contacted with the candidate agent and the level of expression of the polypeptide or the peptide fragment in the sample not contacted with the candidate agent is an indication of an effect of the candidate agent.

77 (New):   The method according to claim 76, wherein said candidate agent is a candidate inhibitory agent.

78 (New):   The method according to claim 76, wherein said candidate agent is a candidate enhancing agent.

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